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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=12; day=17; hr=13; min=47; sec=20; ms=268;]

=====

Reviewer Comments:

<220>

<221> Xaa

<222> (11)..(11)

<223> Xaa is a single amino acid that can be either Met, Ile, or Val.

<400> 3

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Xaa | Pro | Xaa | Xaa | Xaa | Tyr | Xaa | Xaa | Xaa | Xaa | Xaa | Pro | Xaa | Asp |
| 1 | | | 5 | | | | | 10 | | | | | 15 | |

Missing explanation for 'Xaa' at location 15. Please check for similar errors in subsequent sequences.

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

<400> 7

Numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown or Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory,

please indicate that the sequence is synthesized. Please make all
necessary changes, if similar errors detected in subsequent sequences.

Application No: 09510314 Version No: 3.0

Input Set:**Output Set:**

Started: 2008-12-02 17:33:31.534
Finished: 2008-12-02 17:33:35.791
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 257 ms
Total Warnings: 7
Total Errors: 23
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (3) |
| E 341 | 'Xaa' position not defined SEQID (3) POS (15) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (6) |
| W 402 | Undefined organism found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |

Input Set:

Output Set:

Started: 2008-12-02 17:33:31.534
Finished: 2008-12-02 17:33:35.791
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 257 ms
Total Warnings: 7
Total Errors: 23
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

| Error code | Error Description |
|------------|--|
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (43) |
| E 341 | 'Xaa' position not defined SEQID (43) POS (17) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (44) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (44) |

SEQUENCE LISTING

<110> Zhou, Ming-Ming
Aggarwal, Aneel

<120> Methods of Identifying Modulators of Bromodomains

<130> 2459-1-003

<140> 09510314

<141> 2008-12-02

<150> 09/510,314

<151> 2000-02-22

<160> 44

<170> PatentIn version 3.0

<210> 1

<211> 3014

<212> DNA

<213> Homo sapiens

<400> 1

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| gaggctggca | gccgcggca | cgcacacct | gtccgcagtc | ccgaggaaca | tgteccgcagc | 120 |
| cagggcgcg | agcagagtcc | cgggcaggag | aaccaaggga | gggcgtgtgc | tgtggcgcg | 180 |
| gcggcagcgg | cagcggagcc | gctagtcccc | tccctcctgg | gggagcagct | gccgccgctg | 240 |
| ccgccgccgc | caccaccatc | agcgcgcggg | gcccggccag | agcgagccgg | gcgagcgcg | 300 |
| cgctaggggg | agggcggggg | cggggagggg | ggtgggcgaa | gggggcggga | gggcgtgggg | 360 |
| ggagggtctc | gtcttccga | ctaccagagc | ccgagggaga | ccctggcggc | ggcggcggcg | 420 |
| cctgacactc | ggcgccctct | gccgtgtctc | ggggcggcct | gtccgagget | ggcggggccg | 480 |
| ggcggggcgg | ctgcggggca | ggagccgggg | cagggggcgg | gcccggggcg | ctgccccgc | 540 |
| agcctgcggc | gcttccgccc | gcgccccgc | agggctcccc | ctgcgcgct | gccgcgggg | 600 |
| gctcgggcgc | ctgcggtccg | gcgacggcag | tggctgcagc | gggcacggcc | gaaggaccgg | 660 |
| gagggcggtg | ctcgggccga | atcgccgtga | agaaagcgca | actacgctcc | gctccgcggg | 720 |
| ccaagaaact | ggagaaactc | ggagtgtact | ccgcctgcaa | ggccgaggag | tcttgtaaat | 780 |
| gtaatggctg | gaaaaacct | aacctctcac | ccactcccc | cagagccgac | ctgcagcaaa | 840 |
| taattgtcag | tetaacagaa | tctgttcgga | gttgtagcca | tgcctagct | gtcatgttt | 900 |
| cccacctgga | gaatgtgtca | gaggaagaaa | tgaacagact | cctgggaata | gtattggatg | 960 |
| tggaatatct | ctttacctgt | gtccacaagg | aagaagatgc | agataccaaa | caagtttatt | 1020 |
| tctatctatt | taagctcttg | agaaagtcta | ttttacaaag | aggaaaacct | gtggttgaag | 1080 |
| gctctttgga | aaagaaacct | ccatttgaaa | aacctagcat | tgaacagggt | gtgaataact | 1140 |
| ttgtgcagta | caaatttagt | cacctgccag | caaaagaaag | gcaaacaata | gttgagtgg | 1200 |
| caaaaatgtt | cctaaaccgc | atcaactatt | ggcatctgga | ggcaccatct | caacgaagac | 1260 |
| tgcgatctcc | caatgatgat | atttctggat | acaaagagaa | ctacacaagg | tggtctgtgt | 1320 |
| actgcaacgt | gccacagttc | tgcgacagtc | tacctcggt | cgaaaccaca | caggtgtttg | 1380 |
| ggagaacatt | gcttcgctcg | gtcttctactg | ttatgaggcg | acaactcctg | gaacaagcaa | 1440 |
| gacaggaaaa | agataaaactg | cctcttgaaa | aacgaactct | aatcctcact | catttcccaa | 1500 |
| aatttctgtc | catgctagaa | gaagaagtat | atagtcaaaa | ctctcccatc | tgggatcagg | 1560 |
| attttctctc | agcctcttcc | agaaccagcc | agctaggcat | ccaaacagtt | atcaatccac | 1620 |
| ctcctgtggc | tgggacaatt | tcatacaatt | caacctcatc | ttcccttgag | cagccaaaacg | 1680 |
| cagggagcag | cagtcttgcc | tgcaaaacct | cttctggact | tgaggcaaac | ccaggagaaa | 1740 |
| agaggaaaat | gactgattct | catgttcttg | aggaggccaa | gaaacccga | gttatggggg | 1800 |
| atattccgat | ggaattaatc | aacgaggtta | tgtctaccat | cacggaccct | gcagcaatgc | 1860 |

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|------|
| ttggaccaga | gaccaat | ctgtcagcac | actcggccag | ggatgaggcg | gcaaggttgg | 1920 |
| aagagcgcag | gggtgtaatt | gaatttcacg | tgggttgcaa | ttccctcaac | cagaaaccaa | 1980 |
| acaagaagat | cctgatgtgg | ctggttggcc | tacagaacgt | tttctccac | cagctgcccc | 2040 |
| gaatgccaaa | agaatacatc | acacggctcg | tctttgaccc | gaaacacaaa | acccttgctt | 2100 |
| taattaaaga | tggccgtggt | attggtggta | tctgtttccg | tatgttccca | tctcaaggat | 2160 |
| tcacagagat | tgtcttctgt | gctgtaacct | caaagagca | agtcaagggc | tatggaacac | 2220 |
| acctgatgaa | tcatttgaaa | gaatatcaca | taaagcatga | catcctgaac | ttcctcacat | 2280 |
| atgcagatga | atatgcaatt | ggatacttta | agaacacagg | tttctccaaa | gaaattaaaa | 2340 |
| tacctaaaac | caaatatggt | ggctatatca | aggattatga | aggagccact | ttaatgggat | 2400 |
| gtgagctaaa | tccacggatc | ccgtacacag | aattttctgt | catcattaaa | aagcagaagg | 2460 |
| agataattaa | aaaactgatt | gaaagaaaac | aggcacaaat | tcgaaaagtt | taccctggac | 2520 |
| tttcatgttt | taaagatgga | gttcgcacaga | ttcctataga | aagcattcct | ggaattagag | 2580 |
| agacaggctg | gaaaccgagt | ggaaaagaga | aaagtaaaga | gccagagac | cctgaccagc | 2640 |
| tttacagcac | gctcaagagc | atcctccagc | aggtgaagag | ccatcaaagc | gcttggccct | 2700 |
| tcattggaacc | tgtgaagaga | acagaagctc | caggatatta | tgaagttata | aggttcccca | 2760 |
| tggatctgaa | aaccatgagt | gaacgcctca | agaataggta | ctacgtgtct | aagaaattat | 2820 |
| tcattggcaga | cttacagcga | gtctttacca | attgcaaaga | gtacaacgcc | gctgagagtg | 2880 |
| aatactacaa | atgtgccaat | atcctggaga | aattcttctt | cagtaaaatt | aaggaagctg | 2940 |
| gattaattga | caagtgattt | tttttcccc | tctgcttctt | agaaactcac | caagcagtgt | 3000 |
| gcctaaagca | aggt | | | | | 3014 |

<210> 2
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 2

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Ala | Gly | Gly | Ala | Gly | Pro | Gly | Gly | Cys | Gly | Ala | Gly | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Gly | Ala | Gly | Ala | Gly | Pro | Gly | Ala | Leu | Pro | Pro | Gln | Pro | Ala | Ala | Leu |
| | | | | 20 | | | | 25 | | | | | | 30 | |
| | | | | | | | | | | | | | | | |
| Pro | Pro | Ala | Pro | Pro | Gln | Gly | Ser | Pro | Cys | Ala | Ala | Ala | Ala | Gly | Gly |
| | | | | 35 | | | | 40 | | | | | | 45 | |
| | | | | | | | | | | | | | | | |
| Ser | Gly | Ala | Cys | Gly | Pro | Ala | Thr | Ala | Val | Ala | Ala | Ala | Gly | Thr | Ala |
| | | | | 50 | | | | 55 | | | | | 60 | | |
| | | | | | | | | | | | | | | | |
| Glu | Gly | Pro | Gly | Gly | Gly | Gly | Ser | Ala | Arg | Ile | Ala | Val | Lys | Lys | Ala |
| 65 | | | | | | 70 | | | | 75 | | | | | 80 |
| | | | | | | | | | | | | | | | |
| Gln | Leu | Arg | Ser | Ala | Pro | Arg | Ala | Lys | Lys | Leu | Glu | Lys | Leu | Gly | Val |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| | | | | | | | | | | | | | | | |
| Tyr | Ser | Ala | Cys | Lys | Ala | Glu | Glu | Ser | Cys | Lys | Cys | Asn | Gly | Trp | Lys |
| | | | | 100 | | | | 105 | | | | | | 110 | |
| | | | | | | | | | | | | | | | |
| Asn | Pro | Asn | Pro | Ser | Pro | Thr | Pro | Pro | Arg | Ala | Asp | Leu | Gln | Gln | Ile |
| | | | | 115 | | | | 120 | | | | | | 125 | |
| | | | | | | | | | | | | | | | |
| Ile | Val | Ser | Leu | Thr | Glu | Ser | Cys | Arg | Ser | Cys | Ser | His | Ala | Leu | Ala |
| | | | | 130 | | | | 135 | | | | | | 140 | |
| | | | | | | | | | | | | | | | |
| Ala | His | Val | Ser | His | Leu | Glu | Asn | Val | Ser | Glu | Glu | Glu | Met | Asn | Arg |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Gly | Ile | Val | Leu | Asp | Val | Glu | Tyr | Leu | Phe | Thr | Cys | Val | His | 165 | 170 | 175 | |
| Lys | Glu | Glu | Asp | Ala | Asp | Thr | Lys | Gln | Val | Tyr | Phe | Tyr | Leu | Phe | Lys | 180 | 185 | 190 | |
| Leu | Leu | Arg | Lys | Ser | Ile | Leu | Gln | Arg | Gly | Lys | Pro | Val | Val | Glu | Gly | 195 | 200 | 205 | |
| Ser | Leu | Glu | Lys | Lys | Pro | Pro | Phe | Glu | Lys | Pro | Ser | Ile | Glu | Gln | Gly | 210 | 215 | 220 | |
| Val | Asn | Asn | Phe | Val | Gln | Tyr | Lys | Phe | Ser | His | Leu | Pro | Ala | Lys | Glu | 225 | 230 | 235 | 240 |
| Arg | Gln | Thr | Ile | Val | Glu | Leu | Ala | Lys | Met | Phe | Leu | Asn | Arg | Ile | Asn | 245 | 250 | 255 | |
| Tyr | Trp | His | Leu | Glu | Ala | Pro | Ser | Gln | Arg | Arg | Leu | Arg | Ser | Pro | Asn | 260 | 265 | 270 | |
| Asp | Asp | Ile | Ser | Gly | Tyr | Lys | Glu | Asn | Tyr | Thr | Arg | Trp | Leu | Cys | Tyr | 275 | 280 | 285 | |
| Cys | Asn | Val | Pro | Gln | Phe | Cys | Asp | Ser | Leu | Pro | Arg | Tyr | Glu | Thr | Thr | 290 | 295 | 300 | |
| Gln | Val | Phe | Gly | Arg | Thr | Leu | Leu | Arg | Ser | Val | Phe | Thr | Val | Met | Arg | 305 | 310 | 315 | 320 |
| Arg | Gln | Leu | Leu | Glu | Gln | Ala | Arg | Gln | Glu | Lys | Asp | Lys | Leu | Pro | Leu | 325 | 330 | 335 | |
| Glu | Lys | Arg | Thr | Leu | Ile | Leu | Thr | His | Phe | Pro | Lys | Phe | Leu | Ser | Met | 340 | 345 | 350 | |
| Leu | Glu | Glu | Glu | Val | Tyr | Ser | Gln | Asn | Ser | Pro | Ile | Trp | Asp | Gln | Asp | 355 | 360 | 365 | |
| Phe | Leu | Ser | Ala | Ser | Ser | Arg | Thr | Ser | Gln | Leu | Gly | Ile | Gln | Thr | Val | 370 | 375 | 380 | |
| Ile | Asn | Pro | Pro | Pro | Val | Ala | Gly | Thr | Ile | Ser | Tyr | Asn | Ser | Thr | Ser | 385 | 390 | 395 | 400 |
| Ser | Ser | Leu | Glu | Gln | Pro | Asn | Ala | Gly | Ser | Ser | Ser | Pro | Ala | Cys | Lys | 405 | 410 | 415 | |
| Ala | Ser | Ser | Gly | Leu | Glu | Ala | Asn | Pro | Gly | Glu | Lys | Arg | Lys | Met | Thr | 420 | 425 | 430 | |
| Asp | Ser | His | Val | Leu | Glu | Glu | Ala | Lys | Lys | Pro | Arg | Val | Met | Gly | Asp | 435 | 440 | 445 | |
| Ile | Pro | Met | Glu | Leu | Ile | Asn | Glu | Val | Met | Ser | Thr | Ile | Thr | Asp | Pro | 450 | 455 | 460 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Met | Leu | Gly | Pro | Glu | Thr | Asn | Phe | Leu | Ser | Ala | His | Ser | Ala | |
| 465 | | | | | 470 | | | | | 475 | | | | | | 480 |
| Arg | Asp | Glu | Ala | Ala | Arg | Leu | Glu | Glu | Arg | Arg | Gly | Val | Ile | Glu | Phe | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| His | Val | Val | Gly | Asn | Ser | Leu | Asn | Gln | Lys | Pro | Asn | Lys | Lys | Ile | Leu | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| Met | Trp | Leu | Val | Gly | Leu | Gln | Asn | Val | Phe | Ser | His | Gln | Leu | Pro | Arg | |
| | | 515 | | | | | 520 | | | | | 525 | | | | |
| Met | Pro | Lys | Glu | Tyr | Ile | Thr | Arg | Leu | Val | Phe | Asp | Pro | Lys | His | Lys | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| Thr | Leu | Ala | Leu | Ile | Lys | Asp | Gly | Arg | Val | Ile | Gly | Gly | Ile | Cys | Phe | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| Arg | Met | Phe | Pro | Ser | Gln | Gly | Phe | Thr | Glu | Ile | Val | Phe | Cys | Ala | Val | |
| | | | | 565 | | | | | 570 | | | | | 575 | | |
| Thr | Ser | Asn | Glu | Gln | Val | Lys | Gly | Tyr | Gly | Thr | His | Leu | Met | Asn | His | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| Leu | Lys | Glu | Tyr | His | Ile | Lys | His | Asp | Ile | Leu | Asn | Phe | Leu | Thr | Tyr | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| Ala | Asp | Glu | Tyr | Ala | Ile | Gly | Tyr | Phe | Lys | Lys | Gln | Gly | Phe | Ser | Lys | |
| | 610 | | | | | 615 | | | | | 620 | | | | | |
| Glu | Ile | Lys | Ile | Pro | Lys | Thr | Lys | Tyr | Val | Gly | Tyr | Ile | Lys | Asp | Tyr | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| Glu | Gly | Ala | Thr | Leu | Met | Gly | Cys | Glu | Leu | Asn | Pro | Arg | Ile | Pro | Tyr | |
| | | | | 645 | | | | | 650 | | | | | 655 | | |
| Thr | Glu | Phe | Ser | Val | Ile | Ile | Lys | Lys | Gln | Lys | Glu | Ile | Ile | Lys | Lys | |
| | | | 660 | | | | | 665 | | | | | 670 | | | |
| Leu | Ile | Glu | Arg | Lys | Gln | Ala | Gln | Ile | Arg | Lys | Val | Tyr | Pro | Gly | Leu | |
| | | 675 | | | | | 680 | | | | | 685 | | | | |
| Ser | Cys | Phe | Lys | Asp | Gly | Val | Arg | Gln | Ile | Pro | Ile | Glu | Ser | Ile | Pro | |
| | 690 | | | | | 695 | | | | 700 | | | | | | |
| Gly | Ile | Arg | Glu | Thr | Gly | Trp | Lys | Pro | Ser | Gly | Lys | Glu | Lys | Ser | Lys | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| Glu | Pro | Arg | Asp | Pro | Asp | Gln | Leu | Tyr | Ser | Thr | Leu | Lys | Ser | Ile | Leu | |
| | | | | 725 | | | | | 730 | | | | | 735 | | |
| Gln | Gln | Val | Lys | Ser | His | Gln | Ser | Ala | Trp | Pro | Phe | Met | Glu | Pro | Val | |
| | | | 740 | | | | | 745 | | | | | 750 | | | |
| Lys | Arg | Thr | Glu | Ala | Pro | Gly | Tyr | Tyr | Glu | Val | Ile | Arg | Phe | Pro | Met | |
| | | 755 | | | | | 760 | | | | | | 765 | | | |

Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
770 775 780

Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
785 790 795 800

Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
805 810 815

Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
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<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (2)..(4)

<223> Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

<220>

<221> Xaa

<222> (4)..(11)

<223> Xaa is a maximum of eight amino acids. Each of these can be any amino acid. One, two, or three may be missing.

<220>

<221> Xaa

<222> (5)..(5)

<223> Xaa is a single amino acid that is either Pro, Lys, or His.

<220>

<221> Xaa

<222> (6)..(6)

<223> Xaa is any single amino acid.

<220>

<221> Xaa

<222> (8)..(8)

<223> Xaa is a single amino acid that can be either Tyr, Phe, or His.

<220>

<221> Xaa

<222> (9)..(13)

<223> Xaa is 5 amino acids. Each of these can be any amino acid.

<220>

<221> Xaa

<222> (11)..(11)

<223> Xaa is a single amino acid that can be either Met, Ile, or Val.

<400> 3

Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
1 5 10 15

<210> 4

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

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<221> Xaa

<222> (6)..(6)

<223> Xaa represents an acetyl-lysine

<400> 4

Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg
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<210> 5

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> synthetic bromodomain peptide

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<221> Xaa

<222> (8)..(8)

<223> Xaa represents an acetyl lysine.

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Ala Arg Lys Ser Thr Gly Gly Xaa Ala Pro Arg Lys Gln Leu
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<212> PRT

<213> Artificial Sequence

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<221> Xaa

<222> (8)..(8)

<223> Xaa represents an acetyl lysine.

<400> 6

Gln Ser Thr Ser Arg His Lys Xaa Leu Met Phe Lys Thr Glu
1 5 10

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

<400> 7

Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser
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Ile Leu Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu
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Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Ser
35 40 45

Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr
50 55 60

Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn
65 70 75 80

Cys Lys Glu Tyr Asn Ala Pro Glu Ser Glu Tyr Tyr Lys Cys Ala Asn
85 90 95

Ile Leu Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly
100 105 110

<210> 8

<211> 110

<212> PRT

<213> Homo sapiens

<400> 8

Gly Lys Glu Leu Lys Asp Pro Asp Gln Leu Tyr Thr Thr Leu Lys Asn
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Leu Leu Ala Gln Ile Lys Ser His Pro Ser Ala Trp Pro Phe Met Glu
20 25 30

Pro Val Lys Lys Ser Glu Ala Pro Asp Tyr Tyr Glu Val Ile Arg Phe
35 40 45

Pro Ile Asp Leu Lys Thr Met Thr Glu Arg Leu Arg Ser Arg Tyr Tyr
50 55 60

Val Thr Arg Lys Leu Phe Val Ala Asp Leu Gln Arg Val Ile Ala Asn
65 70 75 80

Cys Arg Glu Tyr Asn Pro Pro Asp Ser Glu Tyr Cys Arg Cys Ala Ser
85 90 95

Ala Leu Glu Lys Phe Phe Tyr Phe Lys Leu Lys Glu Gly Gly
100 105 110

<210> 9
<211> 109
<212> PRT
<213> Tetrahymena thermophila

<400> 9

Leu Lys Lys Ser Lys Glu Arg Ser Phe Asn Leu Gln Cys Ala Asn Val
1 5 10 15

Ile Glu Asn Met Lys Arg His Lys Gln Ser Trp Pro Phe Leu Asp Pro
20 25 30

Val Asn Lys Asp Asp Val Pro Asp Tyr Tyr Asp Val Ile Thr Asp Pro
35 40 45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val
50 55 60

Asp Lys Asp Gln Phe Ile Lys Asp Val Lys Arg Ile Phe Thr Asn Ala
65 70 75 80

Lys Ile Tyr Asn Gln Pro Asp Thr Ile Tyr Tyr Lys Ala Ala Lys Glu
85 90 95

Leu Glu Asp Phe Val Glu Pro Tyr Leu Thr Lys Leu Lys
100 105

<210> 10
<211> 109
<212> PRT
<213> Saccharomyces cerevisiae

<400> 10

Ala Gln Arg Pro Lys Arg Gly Pro His Asp Ala Ala Ile Gln Asn Ile
1 5 10 15

Leu Thr Glu Leu Gln Asn His Ala Ala Ala Trp Pro Phe Leu Gln Pro

20

25

30

Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro
 35 40 45

Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln
 50 55 60

Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys
 65 70 75 80

Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg
 85 90 95

Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro
 100 105

<210> 11

<211> 112

<212> PRT

<213> Homo sapiens

<400> 11

Lys Lys Ile Phe Lys Pro Glu Glu Leu Arg Gln Ala Leu Met Pro Thr
 1 5 10 15

Leu Glu Ala Leu Tyr Arg Gln Asp Pro Glu Ser Leu Pro Phe Arg Gln
 20 25 30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr